



hSu(fu) 1 MAELRPSGAPGTAPPAPGPTAPPAFASLFPFGLHAIYGECCRLYPDQPNPLQVTAIVKY
dSu(fu) 1MAEANLDKKPEVKP..PPGLKAIIDHLGQVYPNQPNPLQVTTLLKY

hSu(fu) 61 WLGGPDPPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTGDPSPGFGFEL
dSu(fu) 45 WLGQQDPLDYISMYKFPDVRNVPPHWHYISFGLSDLHGDERVHLREEGVTRSGMGFEL

hSu(fu) 121 LKR...ETGESA..PPTWPAELMQGLARYVFQSENTFCSGDHVSWSHSPLD.
dSu(fu) 105 LAKTEIELKQQIENPEKQORAPTWPANLLQAIGRYCFQTCGNGLCFGDNIPWKRSLDYG

hSu(fu) 169 NSESRIQHMLLTEDPQMOPVQTPFGVVTFLQIVGVCTEELHSAQQWNGQGILELRTVPI
dSu(fu) 165 STTSKLNLLVAQDPQLGCDTPTGTVDFCQIVGVFDDELEQASRWNGRGVLLNFLRQDMQ

hSu(fu) 229 AGGPWLITDMRRGETIFEIDPHLQERVDKGIEIDTGSNLSGVSAKCAWDDL SRPPEDDEDS
dSu(fu) 225 TGGDWLVTNMDRQMSVFELFPETLLNLQDDLEKQGSDDL AGVNA DFSFRELKPTKEVKEE.

hSu(fu) 289 RSICIGTQPRRLSGKDT[EQIR]ETLRRGLEINSK[PVL]PPINPQRQ[NGLA]H DRA[PSRKDSLE
dSu(fu) 284 ...VDFQALSEKCANDE[NRQLTDTQMK-REEPSFPQSMSSMSSN]SL-HKSCPL...DFQ

hSu(fu) 349 SDSSTAIIIPHELIRTRQ[LESVHLKFNQESGALIP]CLRG[RL]HGRHF[SITGDM]AITF
dSu(fu) 335 AQAPNCI.....SLDGEITLAPGVAKYLLLAIKDRIRHGRHF...AQHLALT

hSu(fu) 409 VSTGV[EG]AFA[TEEHP]YAAHGPWLQL
dSu(fu) 384 VAESVTGSAVTVNEPYGVLYWIQVLI PDELVPRLMEDFCAGLDEKCEPKERLELEWPD

hSu(fu) 444 KNLKLIIDQPEPVLPMSLDAAPLKM

FIG.-1

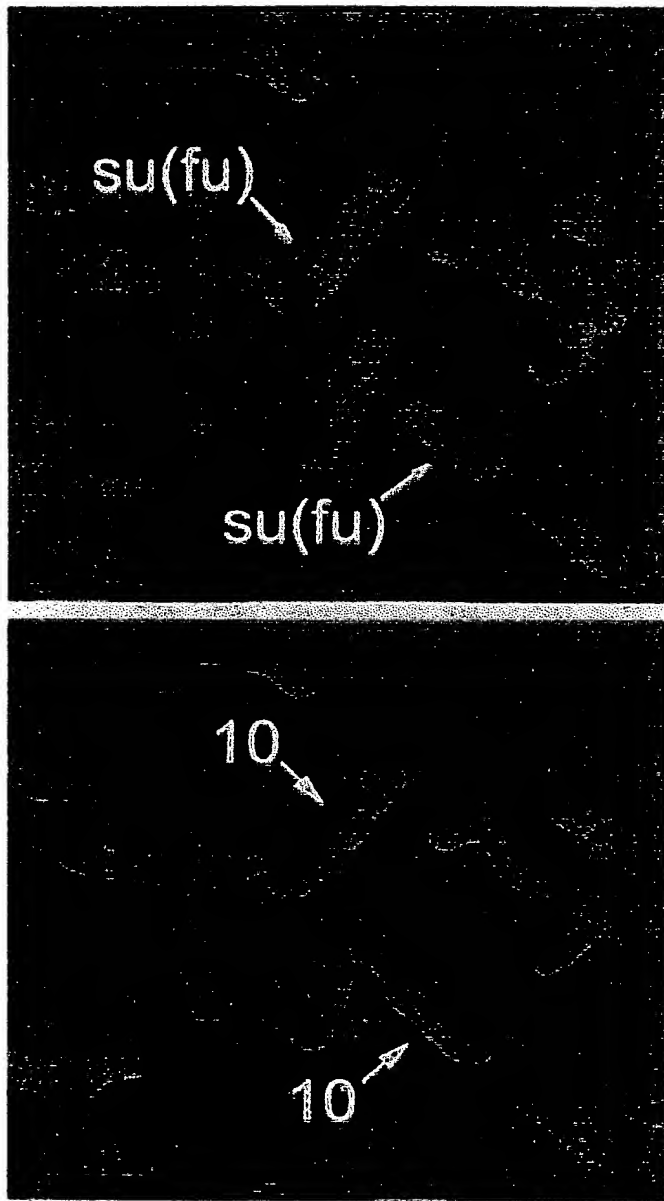


FIG._2A

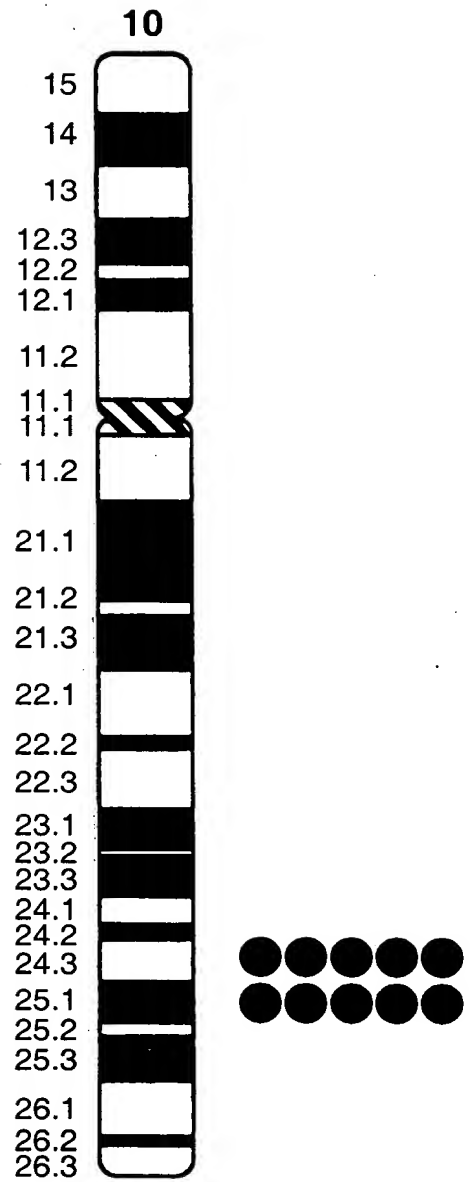


FIG._2B

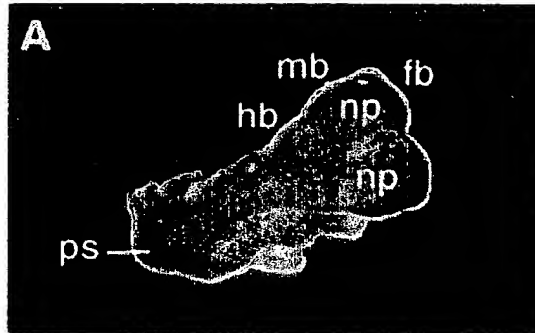


FIG._3A

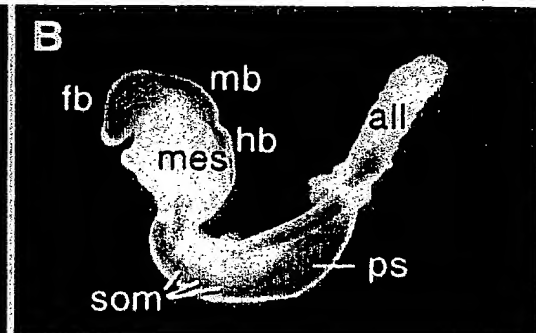


FIG._3B

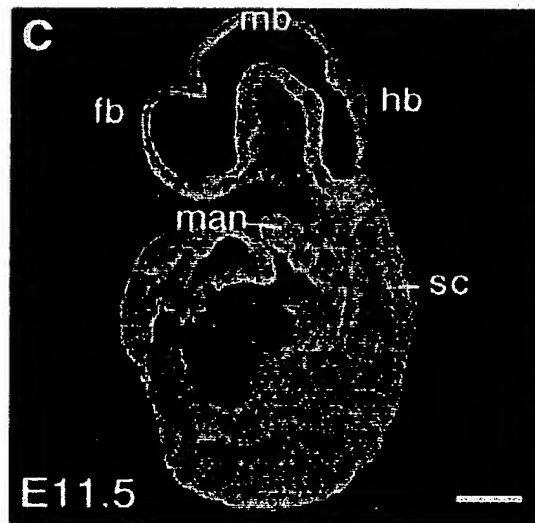


FIG._3C

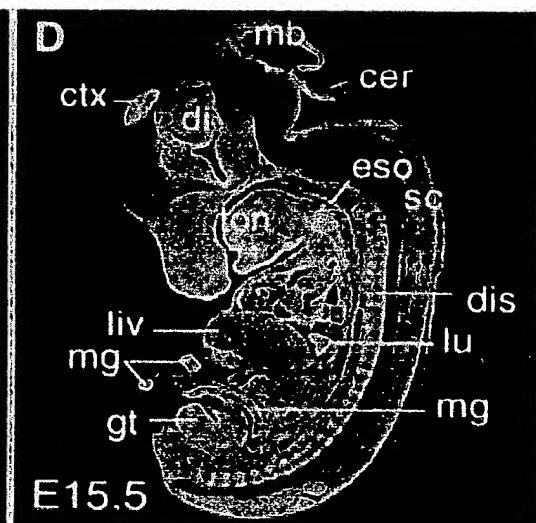


FIG._3D



FIG._3E

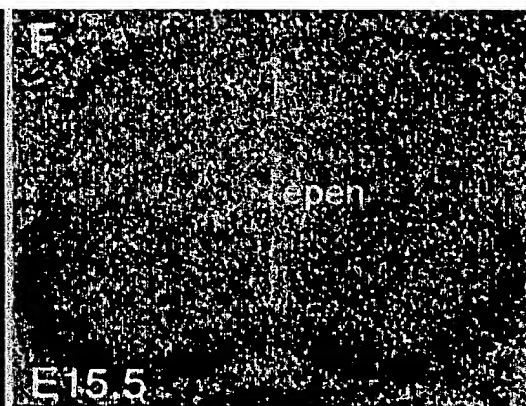


FIG._3F

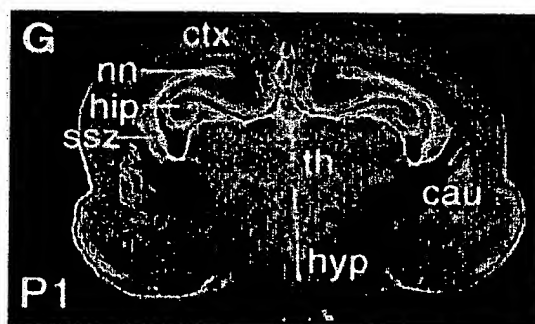


FIG._3G

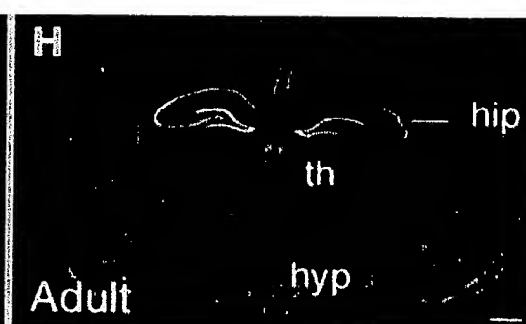


FIG._3H

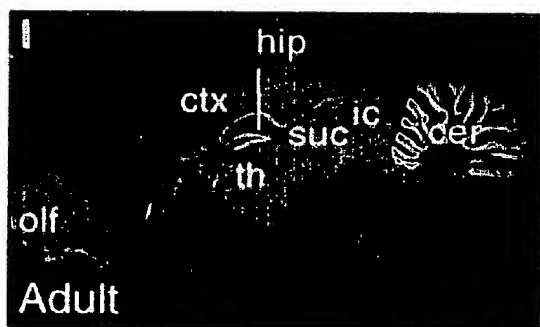


FIG._3I

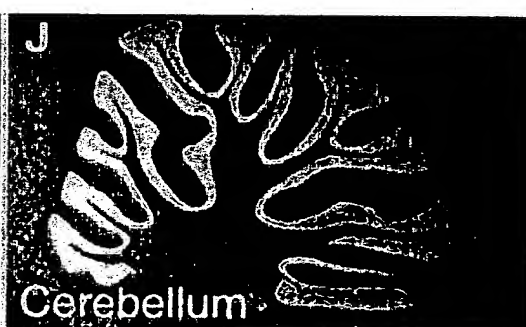


FIG._3J

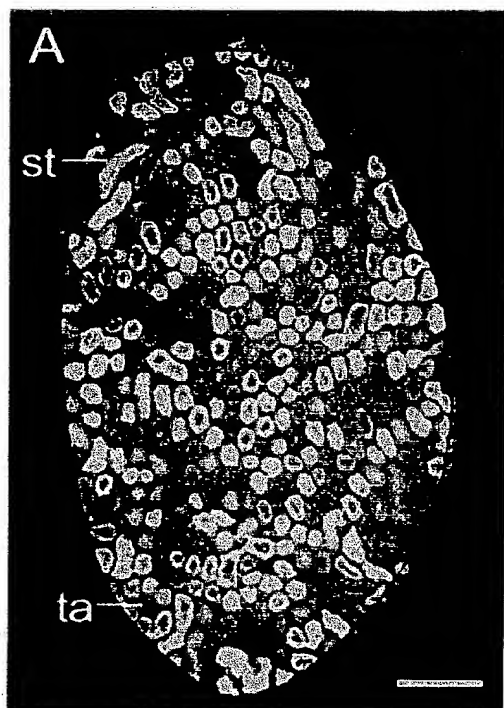


FIG._4A



FIG._4B

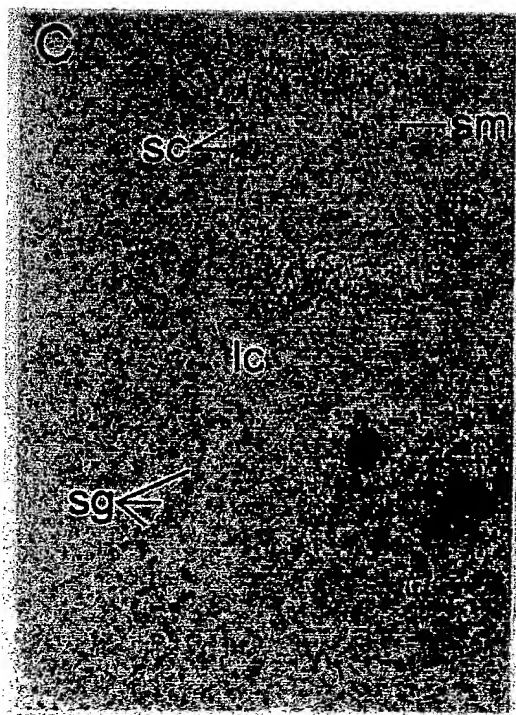


FIG._4C

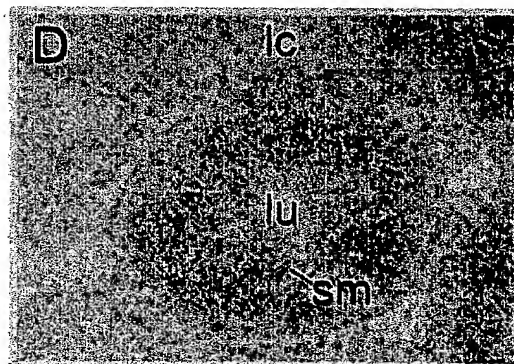


FIG._4D

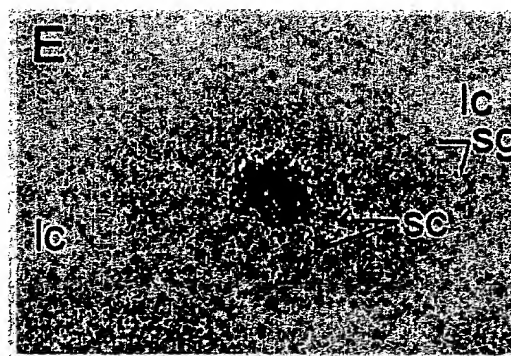


FIG._4E

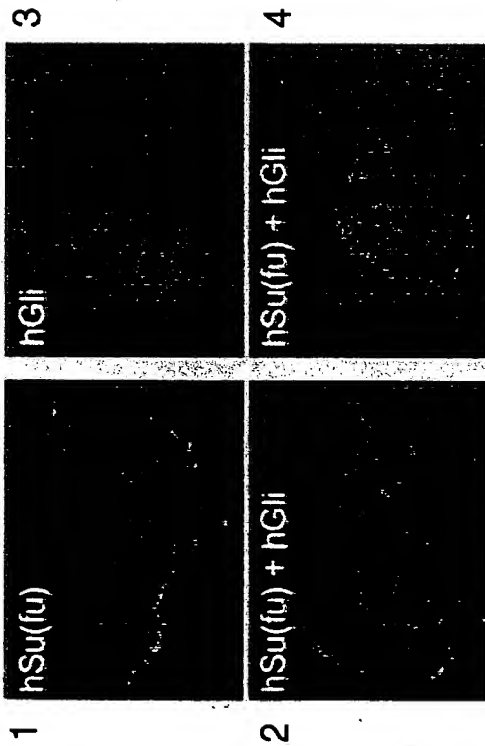


FIG. 5A

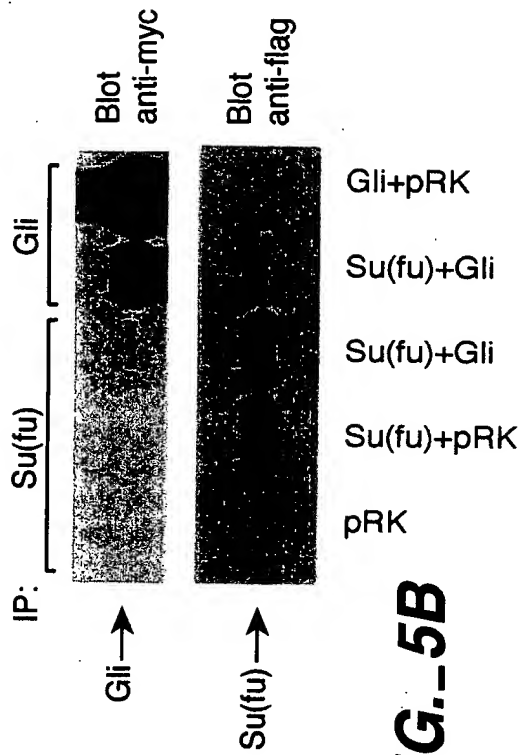


FIG. 5B

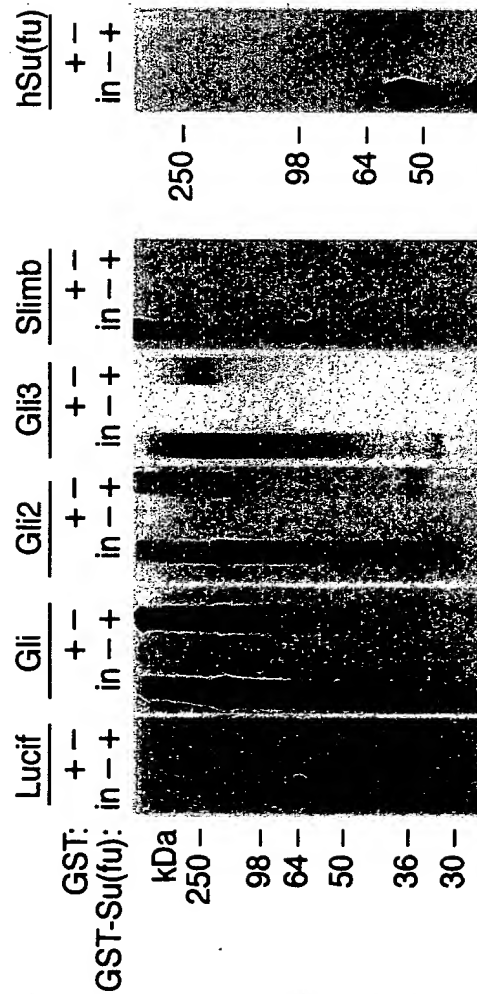


FIG. 5C

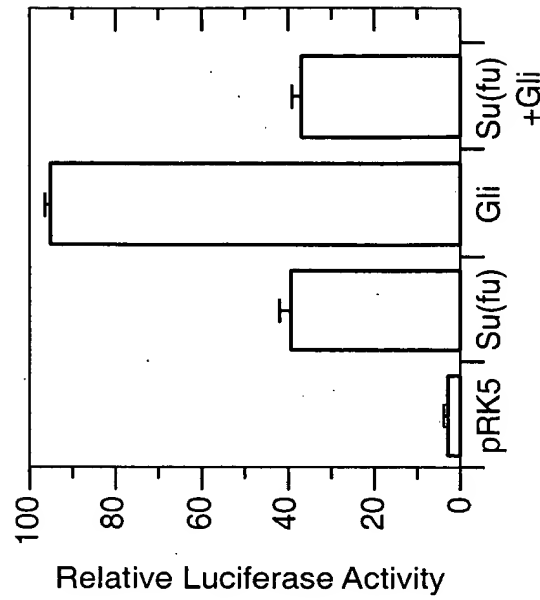


FIG. 5D

1 CCCGCTGGCC CGTCAGTGCT CTCCCGCTCG TTTGCCCTCT CCAGTTCCCC CAGTGCCTGC CCTAGGCACC CGATGGCGG AGCTGGCGC TAGCGGCGCC
GGGCGACCGG GCAGTCACGA GAGGGGCAGC AAACGGGAGA GGTCAAGGG GTCACGGACG GGATGCGTGG GGCTACCGCC TCGACGCGG ATCGCCGCGG
M A E L R P S G A
^orf
^MET

101 CCCGCCCCCA CCGCGCCCCC GGCCCTTGGC CCGACTGCCC CCCGGGCTT CGCTTCGCTC TTTCCTCCCGG GACTGCACGC CATCTACGGA GAGTGCAGCC
GGGCGGGGT GCGCGGGGG CCGGGGACCG GGCTGACGGG GGGGCGGAA CGGAAGCGAG AAAGGGGCC CTGACGTGCG GTAGATGCTT CTCACGGCGG
10 P G P T A P P A P G P T A P P A F A S L F P P G L H A I Y G E C R R
201 GCCTTTACCC TGACCAGCCG AACCCGCTCC AGGTTACCGC TATCGTCAAG TACTGGTTGG GTGGCCCCAGA CCCCTTGGAC TATGTTAGCA TGTACAGGAA
CGGAAATGG ACTGGTCGGC TTGGGCGAGG TCCAATGGC ATAGCAGTTC ATGACCAACC CACCGGCTCT GGGGAACCTG ATACAATCGT ACATGTCCTT
44 L Y P D Q P N P L Q V T A I V K Y W L G G P D P L D Y V S M Y R N
301 TGTGGGGAGC CTTCTGCTA ACATCCCCGA GCACTGGCAC TACATCAGCT TCGGCCCTGAG TGATCTCTAT GGTGACAACA GAGTCCATGA GTTACAGGA
ACACCCCTCG GGAAGACGAT TGTAGGGGCT CGTGACCGTG ATGTAGTCCA AGCCGGACTC ACTAGAGATA CCACCTGTTGT CTCAGGTACT CAAATGTCCT
77 V G S P S A N I P E H W H Y I S F G L S D L Y G D N R V H E F T G
401 ACAGATGGAC CTAGTGGTTT TGGCTTTGAG TTGACCTTTC GTCTGAAGAG AGAACTGGG GAGTCTGCCC CACCAACATG GCGCGCAGAG TTAATGCAGG
TGCTACCTG GATCACCAAA ACCGAACTC AACTGGAAAG CAGACTTCTC TCTTTGACCC CTCAGACGGG GTGGTTGTAC CGGGCGTCTC AATTACGTCC
110 T D G P S G F G F E L T F R L K R E T G E S A P P T W P A E L M Q G
501 GCTTGGCAGC ATACGTGTTT CAGTCAGAGA ACACCTTCTG CAGTGGGGAC CATGTGTCCT GGCACAGCCC TTTGGATAAC AGTGAGTCAA GAATTCAGCA
CGAACCGTGC TATGCACAAG GTCAGTCTCT TGTGGAAGAC GTCACCCCTG GTACACAGGA CCGTGTGCGG AAACCTATTG TCACTCAGTT CTTAAGTCTGT
144 L A R Y V F Q S E N T F C S G D H V S W H S P L D N S E S R I Q H
601 CATGCTGCTG ACAGAGGACC CACAGATGCA GCGCGTGCAG ACACCTTTG GGGTAGTTAC CTTCTCTCCAG ATCGTTGGTG TCTGCACTGA AGAGCTACAC
GTACGACGAC TGTCTCTCTG GTGCTACGT CCGGCACGTC TGTGGGAAAC CCCATCAATG GAAGGAGGTC TAGCAACAC AGACGTGACT TCTCGATGTG
177 M L L T E D P Q M Q P V Q T P F G V V T F L Q I V G V C T E E L H
701 TCAGCCCAGC AGTGAACCG GCAGGGCATC CTGGAGCTGC TCGGACAGT GCCTATTGCT GCGGGCCCCCT GGCTGATAAC TGACATGCGG AGGGGAGAGA
AGTCGGGTG TCACCTTGCC CGTCCCGTAG GACCTCGACG ACGCTGTCA CGGATAACGA CCGCCGGGGA CCGACTATTG ACTGTACGCC TCCCCTCTCT
210 S A Q Q W N G Q G I L E L L R T V P I A G G P W L I T D M R R G E T

FIG._6A

801 CCAATATTGA GATCGATCCA CACCTGCAAG AGAGAGTTGA CAAAGGCATC GAGACAGATG GCTCCAACCT GAGTGGTGT AGTGCCAAGT GTGCCTGGGA
GGTATAAACT CTAGCTAGGT GTGGACGTTT TCTCTCAACT GTTTCGGTAG CTCTGTCTAC CGAGGTTGGA CTCACCACAG TCACGGTTCA CACGGACCCCT
244 I F E I D P H L Q E R V D K G I E T D G S N L S G V S A K C A W D
901 TGACCTGAGC CGGCCCCCG AGGATGACGA GGACAGCCGG AGCATCTGCA TCGGCACACA GCCCCGGCGA CTCTCTGGCA AAGACACAGA GCAGATCCGG
ACTGGAAGTC GCGGGGGGGC TCCTACTGCT CCTGTCTGGC TCCTAGACGT AGCCGTGTGT CCGGGCCGCT GAGAGACCGT TTCTGTGTCT CGTCTAGGCC
277 D L S R P P E D D E D S R S I C I G T Q P R R L S G K D T E Q I R
1001 GAGACCCCTGA GGAGAGGACT CGAGATCAAC AGCAAAACCTG TCCTTCCACC AATCAACCCCT CAGCGGCAGA ATGGCCCTCG CCACGACCGG GCCCCGAGCC
CTCTGGGACT CCTCTCCTGA GCTCTAGTTG TCGTTTGGAC AGGAAGGTGG TTAGTTGGGA GTCCCGCTCT TACCGGAGCG GGTGCTGGCC CCGGGCTCGG
310 E T L R R G L E I N S K P V L P P I N P Q R Q N G L A H D R A P S R
1101 GCAAAGACAG CCTGGAAAGT GACAGCTCCA CGGCCATCAT TCCCCATGAG CTGATTTCGA CGCGGCAGCT TGAGAGCGTA CATCTGAAAT TCAACCAGGA
CGTTTCTGTC GGACCTTTCA CTGTCGAGGT GCGGTAGTA AGGGTACTC GACTAAGCGT GCGCGCTCGA ACTCTCGCAT GTAGACTTTA AGTTGGTCTCT
344 K D S L E S D S S T A I I P H E L I R T R Q L E S V H L K F N Q E
1201 GTCCGGAGCC CTCATTCTCT TCTGCCCTAAG GCGCAGGCTC CTGCATGGAC GGCACCTTAC ATATAAAAGT ATCACAGGTG ACATGGCCAT CACGTTTGT
CAGGCCTCGG GAGTAAGGAG AGACGGATTC CCCGTCCGAG GACGTACCTG CCGTGAAATG TATATTTTCA TAGTGTCCAC TGTACCGGTA GTGCAAAACAG
377 S G A L I P L C L R G R L L H G R H F T Y K S I T G D M A I T F V
1301 TCCACGGGAG TGAAGGCGC CTTTGCCACT GAGGAGCATC CTTACGCGGC TCATGGACCC TGTTTACAAC TCTGAACCTA TCCTCGGAGC TCTGCCCTCC
AGGTGCCCTC ACCTTCCGCG GAAACGGTGA CTCCTCGTAG GAATGCGCG AGTACCTGG ACCAATGTTG AGACTTGGAT AGGAGCCTCG AGACGGGAGG
410 S T G V E G A F A T E E H P Y A A H G P W L Q L O
1401 CGTCCTGGAA CGTCTTTCTG CCCTGAGGAG AGGTTAGTCA GCATCTCCAA TTTTCAGCAG CTCAGAAGCC TTGGCCCCCA CAGGACTTCG CAGATGTCAC
GCAGGACCTT GCAGAAAGAC GGGACTCCTC TCCCATCAGT CGTAGAGGTT AAAAGTCGTC GAGTTCTGG AACCGGGGT GTCTGAAGC GTCTACAGTG
1501 ATTGCCCCCTC AGTCCCCTGA ATGCCCTTCG GACCCAAACC CAATTCCCCA AGCCCCCTGAC CCCCTAGCTG CCGGGGTTC CACTCCCAGT GCCACAACCC
TAACGGGGAG TCAGGGGACT TACGGGAAGC CTGGGTGGG GTTAAGGGGT TCGGGGACTG GGGATCGAC GGCCCCAAGG GTGAGGGTCA CCGTGTGGG
1601 CCTCACCTCC CCTGGCAGCC CCTCAGGAG CCTGAGGCC AGCACCCGCT GGCTCCCCAG CACATGGTCC CCTCCCATGG GCTGTGCCC AGGGAACCGG
GGAGTGGAG GGACCGTCGG GGAGTCGCTC GGACTCCGG TCGTGGGCGA CCGAGGGGTC GTGTACCAGG GGAGGGTACC CGACAACGGG TCCCTTGGCC
1701 GGCGGGTGG GAACGAGCTG CTGGCCTCGG CATGTTTCAA TAAAGTTGCT GTGCTGGGAG
CCGCGCCACC CTTGCTCGAC GACCGGAGCC GTACAAAGTT ATTTCAACGA CACGACCTC

FIG. 6B

1 GGACTGCXTG CCATAGGGGT TTCCCGGXTC CCACCGGXC CCCGGCCCAT GCCXXACTGC CCCXCGXCC TTAXCATCTX TCTTTCCAX GGGACTGCAC
CCTGACGXAC GGTATCGCCA AAGGGGCXAG GGTGGCGCXG GGGCCGGGTA CGGXXTGACG GGGXGCGXGG AATXGTAGAX AGAAAGGGTX CCCTGACGTG

101 GCCATCTACG GAGAGTGCCG CCGCXTTTAX CCTTACCAGC CGAACCCGCT CCAGGTTACC GCTATCGTCA AGTACTGGTT GGGTGGCCCA GACCCCTTGG
CGGTAGATGC CTCTCAGGC GCGXAAATX GGAATGGTCG GCTTGGGCGA GTTCCAATGG CGATAGCAGT TCATGACCAA CCCACCGGGT CTGGGGAACC

201 ACTATGTTAG CATGTACAGG AATGTGGGA GCCCTTCTGC TAACATCCC GAGCACTGGC ACTACATCAG CTTCGGCCTG AGTGATCTCT ATGGTGACAA
TGATACAATC GTACATGTCC TTACACCCCT CGGGAAGACG ATTGTAGGGG CTCTGACCG TGATGTAGTC GAAGCCGGAC TCACCTAGAGA TACCCTGTT

301 CAGAGTCCAT GAAGTTTACA GGAACAGATG GACCTAGTGG TTTTGT
GTCTCAGGTA CTTCAAATGT CCTTGTCTAC CTGGATCACC AAAACA

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FIG.-7



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1 GAGAGTGTCTG CCGCCTCTAC CCTGACCAGC CGAACCCGCT CCAGGTTACC CTATCGTCA
61 AGTACTGGTT GGGTGGTCCG GACCCCTTGG ACTATGTTAG CATGTACAGG ACATGGGGA
121 GTCCTTCTGC CAACATCCCT GAGCACTGGC ACTACATCAG CTTTGGCCTG GTGATCTCT
181 ATGGTGACAA CAGAGTCCAT GAGTTTACAG GAACAGACGG ACCAAGTGA TTGGCTTTG
241 AGTTGACGTT TCGTCTGAAG AGAGAACTG GGGAG

FIG._8

1 GGACTGCNTG CCATAGCGGT TTCCCCGNTC CCACCGCGNC CCCGGCCCAT GCCNNACTGC
61 CCCCNCGNCC TTANCATCTN TCTTTCCCAN GGGACTGCAC GCCATCTACG GAGAGTGCCG
121 CCGCNTTTAN CCTTACCAGC CGAACCCGCT CCAGGTTACC GCTATCGTCA AGTACTGGTT
181 GGGTGGCCCA GACCCCTTGG ACTATGTTAG CATGTACAGG AATGTGGGGA GCCCTTCTGC
241 TAACATCCCC GAGCACTGGC ACTACATCAG CTTGGCCTG AGTGATCTCT ATGGTGACAA
301 CAGAGTCCAT GAAGTTTACA GGAACAGATG GACCTAGTGG TTTTGT

FIG._9

MAELRPSGAPGPTAPPAPGPTAPPAPAFASLFPPGLHAIYGECCRRLYPDQPNPLQVTAIVKY
WLGGPDPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPGSGFGFEL
TFRLKRETGESAPPTWPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIOHMLLT
EDPQMOPVQTPFGVVTFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRR
GETIFEIDPHLQERVDKGIETDGSNLSGVSACAWDDLSRPPEDDEDSRSICIGTQPRRL
SGKDTEQIRETLRRGLEINSKPVLPPIPNQRQNGLAHDRAPSRKDSLESDSSTAIIPHEL
IRTRQLESVHLKFNQESGALIPCLRGRLHGRHFTYKSITGDMAITFVSTGVEGAFATE
EHPYAAHGPWLQLDYKDDDDK

FIG._10

MSPILGWYKIKGLVQPTRLLLEYLEEKYEELHYERDEGDKWRNKKFELGLEFPNLPYYID
GDVKLTQSMAIIRYIADKHNMLGGCPKERAESMLGAVLDIRYGVSRAYSXDFETLKV
DFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFK
KRIEAIPOIDKYLKSSKYIAWPLQGWQATFGGGDHPKSDLVPRGSAELRPSGAPGPTAP
PAPGPTAPPAPAFASLFPPGLHAIYGECCRRLYPDQPNPLQVTAIVKYWLGGPDPLDYVSMYR
NVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPGSGFGFELTFRLKRETGESAPPT
WPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIOHMLLTEDPQMOPVQTPFGVV
TFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRRGETIFEIDPHLQERV
DKGIETDGSNLSGVSACAWDDLSRPPEDDEDSRSICIGTQPRRLSGKDTEQIRETLRRG
LEINSKPVLPPIPNQRQNGLAHDRAPSRKDSLESDSSTAIIPHELIRTRQLESVHLKFNQ
ESGALIPCLRGRLHGRHFTYKSITGDMAITFVSTGVEGAFATEEHPYAAHGPWLQ

FIG._11

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